

GenCode version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:30:12, Search time 18.9429 seconds
(without alignments)
28.464 million cells updated/s/seq

Title: US-09-856-070-19
Perfect score: 65
Sequence: 1 KEELMLRLQDYEE 13

Scoring table: BIOSUM62
Gapop 10 0 : Gapext 0.5

Searched: 112892 seqs, 41475328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	580	P31976	bos taurus
2	65	100.0	585	P15311	homo sapien
3	62	95.4	585	E2RI_MOUSE	mus musculus
4	44	67.7	886	RA50_SULAC	sulfolobus
5	43	66.2	715	BHS2_BRARE	brachydanio
6	41	64.1	365	P211_SCHPO	schistosom
7	40	61.5	576	MORS_HUMAN	homo sapien
8	40	61.5	576	MOES_PIG	mus musculus
9	40	61.5	583	RADI_HUMAN	homo sapien
10	40	61.5	583	RADI_MOUSE	mus musculus
11	40	61.5	583	RADI_PIG	sus scrofa
12	40	61.5	721	BHS2_HUMAN	homo sapien
13	40	61.5	721	BHS2_MOUSE	mus musculus
14	40	61.5	721	BHS2_PAT	rat
15	39	60.0	199	COAE_CLOPE	clostridium
16	39	60.0	315	Y203_AQUAE	aquifex aer
17	39	60.0	435	P274_HUMAN	homo sapien
18	39	60.0	880	RA50_PVEAR	pyrococcus
19	38	58.5	467	INVO_MOUSE	mus musculus
20	38	58.5	756	EFER_HUMAN	homo sapien
21	37	56.9	303	CHEV_BAGSU	bagu
22	37	56.9	370	SELD_DZGDI	dictyostell
23	37	56.9	404	EX71_PUSNN	pus
24	37	56.9	533	SERA_HUMAN	homo sapien
25	37	56.9	533	SERA_PAT	rat
26	37	56.9	576	MOES_MOUSE	mus musculus
27	37	56.9	622	AMT3_CAEEL	caenorhabdi
28	37	56.9	1005	RA50_MET7A	metaphano
29	37	56.9	2472	SVCN_HUMAN	homo sapien
30	37	56.9	2472	SVCN_PAT	rat
31	37	56.9	2477	SVCN_CHICK	gallus gall
32	36.5	56.2	565	LUC1_PHOXY	pholius py
33	36	55.4	320	HLPI_HUMAN	homo sapien

RESULT 1

ID	ENTRY	BOVIN	STANDARD	PRT	580 AA
AC	P31976				
DI	01-JUL-1993	(Rel. 26, Created)			
DI	01-JUL-1993	(Rel. 26, Last sequence update)			
ET	16-OCT-2001	(Rel. 42, Last annotation update)			
DE	Erzin (P81) (Cytochrome) (Villin 2).				
GN	VIL2.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID-9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Brain;				
RA	Bergson C.M., Zhao H., Saljoh K., Duman R.S., Nestler E.J.;				
RI	"Erzin and osteonectin, two proteins associated with cell shape and				
RI	growth, are enriched in the locus coeruleus.";				
RL	Mo1 Cell Neurosci 4:64-73(1993).				
RN	[2]				
RP	SEQUENCE OF 1-15 AND 126-140.				
RC	TISSUE-Kidney;				
FA	MEDLINE-67236137; PubMed-8660651;				
EX	Galat A., Gerbod M.C., Boquet F., Riviere S.;				
PT	"Proteins and their amino acid compositions: uniqueness, variability,				
PT	and applications.";				
RI	Arch. Biochem. Biophys. 330:229-237(1996).				
CC	-!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL				
CC	STRUCTURES TO THE PLASMA MEMBRANE.				
CC	-!- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN				
CC	(CYTOPLASMIC SIDE).				
CC	-!- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.				
CC	-!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.				
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CC	or send an email to license@isb-sib.ch).				
CC	EMBL: M98498; AAA30510.1; ..				
DR	InterPro: IP000294; Band 4.1.				
DR	InterPro: IP000798; P7/rad/moesin.				
DR	Pfam: PF00173; Band 4.1; 1.				
DR	PRINTS: PF00769; ERM; 1.				
DR	SMART: SM00935; BAND41.				
DR	SMART: SM00295; B41; 1.				
DR	PROSITE: PS00660; BAND_41_1; 1.				
DR	PROSITE: PS00661; BAND_41_2; 1.				
DR	PROSITE: PS00657; BAND_41_3; 1.				
KW	Structural protein, Cytoskeleton, Phosphorylation.				
FT	INIT_MET 0 0				

P48677 carassius a
P47819 rattus norv
P32729 torpedo gal
P32148 saccharomyc
P19013 homo sapien
P04264 homo sapien
P35908 homo sapien
P34796 bacillus su
P12814 homo sapien
G921p2 rattus norv
P02562 eryctolagus
G25577 helicobacte

ALIGNMENTS

CC -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
 CC EPITHELIAL CELLS.
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
 CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X60671; CAA43086.1;
 DR PIR: B41129; B41129.
 DR MGI: MGI:98931; V112.
 DR InterPro: IPR000299; Hand.4.1.
 DR InterPro: IPR000798; Ez/rad/moesin.
 DR Pfam: PF00473; Band_41; 1.
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PR00945; HAND41.
 DR SMART: SM00295; B41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 KW Structural protein; Cytoskeleton; Phosphorylation.
 FT INIT_MET 0 0 HY SIMILARITY.
 FT DOMAIN 57 224 HAND 4.1-LIKE.
 FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR)
 FT MOD_RES 353 353 (BY SIMILARITY).
 FT MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
 FT MOD_RES 353 353 (BY SIMILARITY).
 FT MOD_RES 353 353 (BY SIMILARITY).
 SQ SEQUENCE 585 AA: 49214 MW: 20577022.2600562 GPC64.
 Query Match 95.4%; Score 62; DB 1; Length 585.
 Best Local Similarity 92.3%; Pred. No. 0; M24.
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELMLRLQDYEE 13
 DB 343 KEELMLRLQDYEE 355
 RESULT 4
 RA50_SULAC
 ID RA50_SULAC STANDARD; PRT: 886 AA.
 AC Q33600;
 DT 16-OCT-2001 (Rel. 40, Created)
 DI 16-OCT-2001 (Rel. 40, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA double-strand break repair rad50 ATPase.
 GN RAD50.
 OS Sulfolobus acidocaldarius.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 CC Sulfolobus.
 CC NCBI_TaxID=2285;
 RN 111
 RP SEQUENCE FROM N.A.
 RC SIRMAL ACCE 33909 / NCBI 11775 / JSM 639.
 FX MEDLINE 92362414; PubMed 9211741;
 RA Elie C., Baucher M.F., Fondral C., Forterre P.
 FT "A protein related to eucaryal and bacterial DNA-motor proteins in the
 RT hyperthermophilic archaean Sulfolobus acidocaldarius.";
 RL J. Mol. Evol. 45:107-114 (1997).
 CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
 CC rad50/mre11 complex possesses single-strand endonuclease activity
 CC and ATP-dependent double-strand-specific exonuclease activity.
 CC Rad50 provides an ATP-dependent control of mre11 by unwinding
 CC and/or repositioning DNA ends into the mre11 active site (Hy
 CC similarity).
 CC -1- SUBUNIT: Forms a complex with mre11 (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
 CC -----

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 CC -----
 DR EMBL: Y10687; CAA71688.1;
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N; 1.
 DR ProDom: PD000006; ABC_transporter; 1.
 KW DNA repair; Hydrolase; ATP-binding; Coiled coil.
 FT NP_BIND 30 37 ATP (BY SIMILARITY).
 FT DOMAIN 174 727 COILED COIL (POTENTIAL).
 SQ SEQUENCE 885 AA: 104857 MW: 6390461403194104 CRC64;
 Query Match 67.7%; Score 44; DB 1; Length 886;
 Best Local Similarity 66.7%; Pred. No. 5.2;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KEELMLRLQDYEE 13
 DB 258 KEELMLRLQDYEE 269
 RESULT 5
 BBS2_HRAE
 ID BBS2_HRAE STANDARD; PRT: 715 AA.
 AC Q98SF7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DI 15-JUN-2002 (Rel. 41, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bardet-Biedl syndrome 2 protein homolog.
 GN BBS2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CC NCBI_TaxID=7955;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE 2118170; PubMed 11285252;
 RA Nishimura D.Y., Searby C.C., Carmi R., Elbedour K., Van Maldergem L.,
 RA Faltus A.R., Lam R.L., P.-W.-J. H. R., Swidjarski E., Bugae K.E.,
 RA Haider N.B., Kwitek-Black A.E., Ying L., Duhl D.M., Gorman S.M.,
 RA Reck E., Tannenberg A., Bonneau P., Biesecker T.G., Tachson S.G.,
 RA Stone E.M., Sheffield V.C.;
 FT "Positional cloning of a novel gene on chromosome 16q causing
 RT Bardet-Biedl syndrome (BBS2).";
 RL Hum. Mol. Genet. 10:865-874 (2001).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF342739; AAC28555.1;
 SQ SEQUENCE 715 AA: 79125 MW: 326770424540090 CRC64;
 Query Match 96.2%; Score 43; DB 1; Length 715;
 Best Local Similarity 61.5%; Pred. No. 6.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KEELMLRLQDYEE 13
 DB 345 KEELMLRLQDYEE 357

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RESULT 6
ID ECTL SCHPO STANDARD: PKT: 365 AA.
AC Q9UT16;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable ethanolamine-phosphate cytidyltransferase (PC 2.7.7.14)
DE (Phosphorylethanolamine transferase) (CIP:phosphoethanolamine
GN SPAC13EL105C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.
OC Schizosaccharomycetes.
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soares J., Peal N., Hayes J., Reher S., Bushan B., Bowman S.,
RA Brooks J., Brown D., Brown S., Chillingworth I., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby I., Howarth S., Hyuckle F. I., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA McInerney P., Moule S., Munnall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkmer E., Aert R., Robben J., Grymonprez B.,
RA Well-jens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt K., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Ielaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dada P.P., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J., Moreno S., Armstrong J., Folsburg S.L.,
RA Cerretti L., Lowe J., McCombie W.R., Paulsen O., Potashkin J.,
RA Shpakovski G.V., Ussey D., Bartlett B.G., Nurse P.,
RT The genome sequence of Schizosaccharomyces pombe.
RE Nature 415:871-880(2002).
CC -1- CATALYTIC ACTIVITY: CTP + ethanolamine phosphate -> diphosphate +
CIP-ethanolamine.
CC -1- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CIP-ETHANOLAMINE SYNTHESIS;
CC SECOND STEP.
CC -1- SIMILARITY: BELONGS TO THE CYTIDYLTRANSFERASE FAMILY.
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EMBL: M59056; AAA3322.1;
DE EMBL, Z98946, CAB46379.1;
DI PIP; A41289; A41289.
DR Aarthus/Ghent-20PAGE; 3515; IFF.
DR Aarthus/Ghent-20PAGE; 3516; IFF.
DR Genew; HNC7373; MSN.
DR MIN; 309845;
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000799; E2/Fad/moesin.
DR Pfam; PF00373; Band 4.1.
DR Pfam; PF00769; ERM; 1.
DR PRINTS; PR00935; BAND41.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS00660; BAND41_1; 1.
DR PROSITE; PS00661; BAND41_2; 1.
DR PROSITE; PS00657; BAND41_3; 1.
DR Structural protein; Cytoskeleton.
KW INIT-MET 0
FT DOMAIN 57 224 BAND 4.1-LIKE.
SQ SEQUENCE 576 AA; 67689 MW; 96CE7C28D5A8176 CRC64;
Query Match 61.5%; Score 40; DB 1; Length 576;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9, Conservative 1, Mismatches 3, Indels 0, Gaps 0;

OY 1 KEELMLRQDYEE 13
I: ||||| |||
Db 333 KORVLRQHYEE 345

RESULT 7
ID MOES_HUMAN STANDARD: PKT: 576 AA.
AC P26038;
DT 01-MAY-1992 (Rel. 22, Created)
DI 01-MAY-1992 (Rel. 23, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Moesin (Membrane organizing extension spike protein).
GN MSN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15; 53-59 AND 413-444.
RX TISSUE-Placenta;
EX MEDLINE=4206843; PubMed=1934289;
RA Lankes W.T., Furthmayr H.,
RT "Moesin: a member of the protein 4.1-talin-c7rin family of proteins.";
RA Proc. Natl. Acad. Sci. U.S.A. 88:8297-8301(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Howden P.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
STRUCTURES TO THE PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: IN ALL TISSUES AND CULTURED CELLS STUDIED.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- DATABASE: NAME-Atlas Genet. Cylogenet. Oncol. Haematol.;
WWW=http://www.infobiogen.fr/services/chronocancer/Genes/MSNID363.html.
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EMBL: M59056; AAA3322.1;
DE EMBL, Z98946, CAB46379.1;
DI PIP; A41289; A41289.
DR Aarthus/Ghent-20PAGE; 3515; IFF.
DR Aarthus/Ghent-20PAGE; 3516; IFF.
DR Genew; HNC7373; MSN.
DR MIN; 309845;
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000799; E2/Fad/moesin.
DR Pfam; PF00373; Band 4.1.
DR Pfam; PF00769; ERM; 1.
DR PRINTS; PR00935; BAND41.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS00660; BAND41_1; 1.
DR PROSITE; PS00661; BAND41_2; 1.
DR PROSITE; PS00657; BAND41_3; 1.
DR Structural protein; Cytoskeleton.
KW INIT-MET 0
FT DOMAIN 57 224 BAND 4.1-LIKE.
SQ SEQUENCE 576 AA; 67689 MW; 96CE7C28D5A8176 CRC64;
Query Match 61.5%; Score 40; DB 1; Length 576;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9, Conservative 1, Mismatches 3, Indels 0, Gaps 0;

OY 1 KEELMLRQDYEE 13
I: ||||| |||
Db 343 KEELMLRQHYEE 355

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CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
CC 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: X60672; CAA44087.1;
DR PIR: A41129; A41129.
DR MGI: MGI:97887; Rdx.
DR InterPro: IPR000299; Band_4.1.
DR Pfam: PF00373; Band_41; 1.
DR PRINTS: PR00935; RAND41.
DR SMART: SM00295; H41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.
FT DOMAIN 58 225 BAND 4.1-LIKE.
FT DOMAIN 470 477 POLY-PRO.
SQ SEQUENCE 583 AA; 68451 MW; 3219A52E7C7B78FE CRC64;

Query Match 61.5%; Score 40; DB 1; Length 583;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERLQYEE 13
| | | | |
DB 344 KEELMERLQYEE 356

RESULT 11
RADI_PIG STANDARD PPT: 583 AA
AC P26044;
DI 01-MAY-1992 (Rel. 22, Created)
DI 01-MAY-1992 (Rel. 22, Last sequence update)
DI 16-OCT-2002 (Rel. 40, Last annotation update)
DE Radixin (Moesin B).
GN RDX.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Catartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9409274; PubMed 8248241;
RA Banks W.F., Schwartz-Albiez P., Furthmayr H.;
RI "Cloning and sequencing of porcine moesin and radixin cDNA and
RI identification of highly conserved domains."
RL Biochim. Biophys. Acta 1216:479-482(1993).
CC 1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE
CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
CC 1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE
CC CELL TO CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE
CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
CC 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: M86444; AAR02865.1;

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DR PIR: S39805; S39805.
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_41; 1.
DR PRINTS: PR00769; ERM; 1.
DR PRINTS: PR00935; RAND41.
DR SMART: SM00295; H41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.
FT DOMAIN 58 225 BAND 4.1-LIKE.
FT DOMAIN 470 477 POLY-PRO.
SQ SEQUENCE 583 AA; 59A1A286DCAF7397 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 583;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERLQYEE 13
| | | | |
DB 344 KEELMERLQYEE 356

RESULT 12
RHS2_HUMAN STANDARD PPT: 721 AA.
AC Q9BXC9; Q96CM0; Q96SN9;
DI 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bardet-Biedl syndrome 2 protein.
GN BBS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. VAPIANT BBS2 GLY-75, AND VAPIANT VAL-123.
RX MEDLINE-21181710; PubMed-11285252;
RA Nishimura P.Y., Searby C.C., Carmi P., Elbedour K., Van Malderghem L.,
RA Fulton A.H., Lam B.L., Powell B.R., Swiderski R.E., Ruzke K.E.,
RA Halder N.R., Kwitek-Black A.E., Ying L., Dahl D.M., Gorman S.M.,
RA Heon E., Iannaccone A., Bonneau D., Biesecker L.G., Jacobson S.G.,
RA Stone E.M., Shellfield V.C.;
PT "Positional cloning of a novel gene on chromosome 16q causing
PT Bardet-Biedl syndrome (BBS2).";
RL Hum. Mol. Genet. 10:865-874(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Naqai K., Suquano S., Shiratori A., Sudo H.,
RA Wajikawa M., Bosvelli T., Kaku Y., Kodaira H., Kondo H., Sudaawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ouo Y., Takiguchi S.,
RA Watanabe S., Kimata K., Matsumi K., Nakamura Y., Nagahara K., Masuko Y.,
RA Yamamoto J., Wakamatsu A., Nishimura T.;
RA Nishimura T., Iwayanagi T.;
PT "NFDG human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Placenta;
RN [4]
RP Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RX MEDLINE-21451214; PubMed-11567139;
RA Katsanis N., Ansley S.J., Hadano J.L., Eichers E.R., Lewis R.A.,
RA Hoskins R.E., Scambler P.J., Davidson W.S., Reales P.L., Lupski J.R.;
PT "Triallelic inheritance in Bardet-Biedl syndrome, a mendelian
PT recessive disorder.";
RL Science 293:2256-2259(2001).
CC 1- TISSUE SPECIFICITY: Widely expressed.

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